SEQUENCE LISTING

| <110> | Hannoufa, Abdelali Hegedus, Dwayne Bate, Nicholas | | | | | | |
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| <120> in Plan | A Repressor-Mediated Regulation System for Control of Gene Expression | | | | | | |
| <130> | 1096.021A | | | | | | |
| <150> | PCT/CA02/00740 | | | | | | |
| <151> | 2002-05-23 | | | | | | |
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| <150> | US 60/292,973 | | | | | | |
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| gtggct | gcct atgttagcaa ccacgtcgtt ccggtaactg agcttcccgg ccttatttcg 120 | | | | | | |
| gatgtt | cata cggcactcag cggaacatcg gcaccggcat cggtggcggt caatgttgaa 180 | | | | | | |
| aagcag | aagc ctgctgtgtc ggttcgcaag tcggttcagg acgatcatat cgtctgtttg 240 | | | | | | |
| gaatgt | ggtg gctcgttcaa gtcgctcaaa cgccacctga cgacgcatca cagcatgacg 300 | | | | | | |

ccggaagaat atcgcgaaaa atgggatctg ccggtcgatt atccgatggt tgctcccgcc 360 tatgccgaag cccgttcgcg gctcgccaag gaaatgggtc tcggtcagcg ccgcaaggcg 420 429 aaccgttga <210> 2 <211> 458 <212> DNA <213> Artificial <220> synthetic ROS optimized for plant codon usage and encoding fusion of ROS and nuclear localization signa <400> atgactgaga ctgcttacgg taacgctcag gatcttcttg ttgagcttac tgctgatatc 60 gttgctgctt acgtttctaa ccacgttgtt cctgttactg agcttcctgg acttatctct 120 gatgttcata ctgcactttc tggaacatct gctcctgctt ctgttgctgt taacgttgag 180 aagcagaagc ctgctgtttc tgttcgtaag tctgttcagg atgatcatat cgtttgtttg 240 gagtgtggtg gttctttcaa gtctctcaag cgtcacctta ctactcatca ctctatgact 300 ccagaggagt atagagagaa gtgggatctt cctgttgatt accctatggt tgctcctgct 360 tacgetgagg ctcgttctcg tctcgctaag gagatgggtc tcggtcagcg tcgtaaggct 420 458 aaccgtccaa aaaagaagcg taaggtctga gagctcgc <210> 3 447 <211> <212> DNA <213> Artificial <220> <223> ROS consensus sequence

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| <400> atgacno | 3 ngara engentaygg naaygenear gayytnytng | tngarytnac | ngcngayath | 60 | | |
| gtngcng | ngcnt aygtnwsnaa ycaygtngtn ccngtnacng | arytnccngg | nytnathwsn | 120 | | |
| gaygtno | ncaya engenytnws nggnaenwsn geneengenw | sngtngcngt | naaygtngar | 180 | | |
| aarcara | raarc engengtnws ngtnmgnaar wsngtnearg | aygaycayat | hgtntgyytn | 240 | | |
| gartgy | yggng gnwsnttyaa rwsnytnaar mgncayytna | cnacncayca | ywsnatgacn | 300 | | |
| ccngarç | rgart aymgngaraa rtgggayytn ccngtngayt | ayccnatggt | ngeneengen | 360 | | |
| taygcng | ngarg cnmgnwsnmg nytngcnaar garatgggny | tnggncarmg | nmgnaargcn | 420 | | |
| aaymgno | nccna araaraarmg naargtn | | | 447 | | |
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| <223> | where n is A or T or G or C | | | | | |
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| | tcct ttcagggcca tttcag | 26 |
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| <400> tatatt | 8 caa tttt | attgta | atata | | | | 25 |
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| <212> | DNA | | | | | | |
| <213> | Artifici | al | | | | | |
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| <223> | ROS-OPDS | oligo | for p74-315 | construct | | | |
| <400> atctcca | 9 actg acgt | aaggga | tgacgcacaa | tcccactatc | cttcgcaaga | cccttcctct | 60 |
| atataat | ata tttc | aatttt | attgtaatat | aacacggggg | actctagag | | 109 |
| <210> | 10 | | | | | | |
| <211> | 113 | | | | | | |
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| | | | | | | | |
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| <400> gatccto | 10 ctag agto | ccccgt | gttatattac | aataaaattg | aaatatatta | tatagaggaa | 60 |
| gggtctt | gcg aagg | atagtg | ggattgtgcg | tcatccctta | cgtcagtgga | gat | 113 |
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| <211> | 107 | | | | | | |
| <212> | DNA | | | | | | |
| <213> | Artifici | al | | | | | |
| | | | | | | | |

.

<220>

| <223> | ROS-OPUS oligo | for p74-31 | 6 construct | | | |
|-----------------|-----------------------|------------|-------------|------------|------------|-----|
| <400> atctcc | 11 actg acgtaaggga | tgacgcacaa | tctatatttc | aattttattg | taatatacta | 60 |
| tataag | gaag ttcatttcat | ttggagagaa | cacgggggac | tctagag | | 107 |
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| <213> | Artificial | | | | | |
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| <220> | | | | | | |
| <223> | ROS-OPUA oligo | for p74-31 | 6 construct | | | |
| <400> | 12 | | | | | |
| gatcct | ctag agtcccccgt | gttctctcca | aatgaaatga | acttccttat | atagtatatt | 60 |
| acaata | aaat tgaaatatag | attgtgcgtc | atcccttacg | tcagtggaga | t | 111 |
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| <212> | DNA | , | | | | |
| <213> | Artificial | | | | | |
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| <223> | ROS-OPPS oligo | for p74-30 | 9 construct | | | |
| <400> | 13 | | | | | |
| atctcc | actg acgtaaggga | tgacgcacaa | tctatatttc | aattttattg | taatatacta | 60 |
| tataat | atat ttcaatttta | ttgtaatata | acacggggga | ctctagag | | 108 |
| | | | | | | |
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| <211> | 112 | | | | | |
| <212> | DNA | | | | | |
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<223> ROS-OPPA oligo for p74-309 construct
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gatcctctag agtcccccgt gttatattac aataaaattg aaatatatta tatagtatat
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tacaataaaa ttgaaatata gattgtgcgt catcccttac gtcagtggag at
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<223> ROS-OP1 oligo for p76-508 construct
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gatcctatat ttcaatttta ttgtaatata gctatatttc aattttattg taatataat
                                                                    59
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cgattatatt acaataaaat tgaaatatag ctatattaca ataaaattga aatatag
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| <220> | | |
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| <223> | sense primer for amplifying Actin2 promoter | |
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| _ | | |
| <210> | 18 | |
| <211> | 24 | |
| <212> | DNA | |
| <213> | Artificial | |
| | | |
| <220> | | |
| <223> | antisense primer for amplifying Actin2 promoter | |
| <400> | 18 agta tcagcctcag ccat | 24 |
| cegace | agea ceageereag ceae | 27 |
| <210> | 19 | |
| <211> | 27 | |
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| | | |
| <220> | | |
| <223> | ROS operator sequence in ipt gene | |
| <400> | 19 | 2.5 |
| tataati | taaa atattaactg tcgcatt | 27 |
| <210> | 20 | |
| <211> | 10 | |
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| <223> | consensus ROS operator sequence | |

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60

120

gatateteca etgaegtaag ggatgaegea caateeeact ateettegea agaeeettee

tctatataat atatttcaat tttattgtaa tataacacgg gggactctag aggatccccg

| ggtggto | cagt cccttatg | 138 |
|------------------|--|-----|
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| <211> | 136 | |
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| <220> | | |
| <223> | p74-316 sequence from EcoRV site to ATG codon of GUS | |
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| ctatata | agg aagttcattt catttggaga gaacacgggg gactctagag gatccccggg | 120 |
| tggtcag | gtcc cttatg | 136 |
| <210> | 24 | |
| <211> | 137 | |
| <212> | DNA | |
| <213> | Artificial | |
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| <220> | | |
| <223> | p74-309 sequence from EcoRV site to ATG codon of GUS | |
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| ctatata | aata tatttcaatt ttattgtaat ataacacggg ggactctaga ggatccccgg | 120 |
| gtggtca | agtc ccttatg | 137 |
| <210> | 25 | |
| <211> | 237 | |
| <212> | DNA | |
| | Artificial | |

<220>

<223> p74-118 sequence from EcoRV site to ATG codon of GUS

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<210> 26

<211> 142

<212> PRT

<213> Agrobacterium tumefaciens

<400> 26

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Thr Ala Asp Ile Val Ala Ala Tyr Val Ser Asn His Val Val Pro Val

Thr Glu Leu Pro Gly Leu Ile Ser Asp Val His Thr Ala Leu Ser Gly

Thr Ser Ala Pro Ala Ser Val Ala Val Asn Val Glu Lys Gln Lys Pro 50

Ala Val Ser Val Arg Lys Ser Val Gln Asp Asp His Ile Val Cys Leu

Glu Cys Gly Gly Ser Phe Lys Ser Leu Lys Arg His Leu Thr Thr His 90

His Ser Met Thr Pro Glu Glu Tyr Arg Glu Lys Trp Asp Leu Pro Val 100

Asp Tyr Pro Met Val Ala Pro Ala Tyr Ala Glu Ala Arg Ser Arg Leu

Ala Lys Glu Met Gly Leu Gly Gln Arg Arg Lys Ala Asn Arg 130 135 140

<210> 27

<211> 149

<212> PRT

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<220>

<223> synthetic-ROS fused to nuclear localization signal

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Met Thr Glu Thr Ala Tyr Gly Asn Ala Gln Asp Leu Leu Val Glu Leu

1 10 15

Thr Ala Asp Ile Val Ala Ala Tyr Val Ser Asn His Val Val Pro Val 20 25 30

Thr Glu Leu Pro Gly Leu Ile Ser Asp Val His Thr Ala Leu Ser Gly 35 40 45

Thr Ser Ala Pro Ala Ser Val Ala Val Asn Val Glu Lys Gln Lys Pro 50 55 60

Ala Val Ser Val Arg Lys Ser Val Gln Asp Asp His Ile Val Cys Leu 65 70 75 80

Glu Cys Gly Gly Ser Phe Lys Ser Leu Lys Arg His Leu Thr Thr His
85 90 95

His Ser Met Thr Pro Glu Glu Tyr Arg Glu Lys Trp Asp Leu Pro Val 100 105 110

Asp Tyr Pro Met Val Ala Pro Ala Tyr Ala Glu Ala Arg Ser Arg Leu 115 120 125

Ala Lys Glu Met Gly Leu Gly Gln Arg Arg Lys Ala Asn Arg Pro Lys 130 135 140

Lys Lys Arg Lys Val 145

<210> 28

<211> 143

<212> PRT

<213> rhizobium elti

<400> 28

Met Thr Asp Met Ala Thr Gly Asn Ala Pro Glu Leu Leu Val Glu Leu 1 5 10 15 Thr Ala Asp Ile Val Ala Ala Tyr Val Ser Asn His Val Val Pro Val
20 25 30

Ser Asp Leu Ala Asn Leu Ile Ser Asp Val His Ser Ala Leu Ser Asn 35 40 45

Thr Ser Val Pro Gln Pro Ala Ala Val Val Glu Lys Gln Lys Pro 50 55 60

Ala Val Ser Val Arg Lys Ser Val Gln Asp Glu Gln Ile Thr Cys Leu 65 70 75 80

Glu Cys Gly Gly Asn Phe Lys Ser Leu Lys Arg His Leu Met Thr His 85 90 95

His Ser Leu Ser Pro Glu Glu Tyr Arg Glu Lys Trp Asp Leu Pro Thr 100 105 110

Asp Tyr Pro Met Val Ala Pro Ala Tyr Ala Glu Ala Arg Ser Arg Leu 115 120 125

Ala Lys Glu Met Gly Leu Gly Gln Arg Arg Lys Arg Gly Arg Gly 130 135 140

<210> 29

<211> 142

<212> PRT

<213> agrobacterium radiobacter

<400> 29

Met Thr Glu Thr Ala Tyr Gly Asn Ala Gln Asp Leu Leu Val Glu Leu

1 10 15

Thr Ala Asp Ile Val Ala Ala Tyr Val Ser Asn His Val Val Pro Val 20 25 30

Thr Glu Leu Pro Gly Leu Ile Ser Asp Val His Thr Ala Leu Ser Gly 35 40 45

Thr Ser Ala Pro Ala Ser Val Ala Val Asn Val Glu Lys Gln Lys Pro 50 55 60

Ala Val Ser Val Arg Lys Ser Val Gln Asp Asp His Ile Val Cys Leu 70 75 80

Glu Cys Gly Gly Ser Phe Lys Ser Leu Lys Arg His Leu Thr Thr His
85 90 95

His Ser Met Thr Pro Glu Glu Tyr Arg Glu Lys Trp Asp Leu Gln Val 100 105 110

Asp Tyr Pro Met Val Ala Pro Ala Tyr Ala Glu Ala Arg Ser Arg Leu

115 120 125

Ala Lys Glu Met Gly Leu Gly Gln Arg Arg Lys Ala Asn Arg 130 135 140

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<211> 143

<212> PRT

<213> rhizobium meliloti

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Met Thr Glu Thr Ser Leu Gly Thr Ser Asn Glu Leu Leu Val Glu Leu 1 5 10 15

Thr Ala Glu Ile Val Ala Ala Tyr Val Ser Asn His Val Val Pro Val
20 25 30

Ala Glu Leu Pro Thr Leu Ile Ala Asp Val His Ser Ala Leu Asn Asn 35 40 45

Thr Thr Ala Pro Ala Pro Val Val Pro Val Glu Lys Pro Lys Pro 50 55 60

Ala Val Ser Val Arg Lys Ser Val Gln Asp Asp Gln Ile Thr Cys Leu 70 75 80

Glu Cys Gly Gly Thr Phe Lys Ser Leu Lys Arg His Leu Met Thr His 85 90 95

His Asn Leu Ser Pro Glu Glu Tyr Arg Asp Lys Trp Asp Leu Pro Ala 100 105 110

Asp Tyr Pro Met Val Ala Pro Ala Tyr Ala Glu Ala Arg Ser Arg Leu 115 120 125

Ala Lys Glu Met Gly Leu Gly Gln Arg Arg Lys Arg Arg Gly Lys 130 135 140

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<211> 47

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<223> potyvirus nuclear localization signal

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<221> x

<222> (12)..(44)

<223> unknown or other amino acid

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Lys Lys Asn Gln Lys His Lys Leu Lys Ala Ala Met Xaa Xaa Xaa Xaa 1 5 10 15

<210> 36

<211> 17

<212> PRT

<213> Xenopus sp.

<400> 36

Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys 1 5 10 15

Leu

<210> 37

<211> 17

<212> PRT

<213> Xenopus sp.

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 Arg
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       17
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 <400> 38
 Lys Arg Lys Thr Glu Glu Glu Ser Pro Leu Lys Asp Lys Asp Ala Lys
                                    10
 Lys
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 <213> Mus sp./Rattus sp.
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 Arg Lys Cys Leu Gln Ala Gly Met Asn'Leu Glu Ala Arg Lys Thr Lys
Lys
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 <213> Homo sapiens
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Lys

<210> 41

<211> 17

<212> PRT

<213> Homo sapiens

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Lys

<210> 42

<211> 17

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<213> Gallus sp.

<400> 42

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Lys

<210> 43

<211> 17

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<213> Homo sapiens

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1 5 10 15

Lys

<210> 44

<211> 17

<212> PRT

<213> Gallus sp.

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Arg Arg Cys Phe Glu Val Arg Val Cys Ala Cys Pro Gly Arg Asp Arg 1 5 10 15

Lys